







[illegible]

```

1  APPLICANT: Steiner, Sabine
2  APPLICANT: Mohr, Christine
3  APPLICANT: Wendland, Jürgen
4  APPLICANT: Koechlin, Philipp
5  APPLICANT: Koechlin, Carline
6  TITLE OF INVENTION: STRUCTURE OF ASHVA GAGETCTI
7  TITLE OF INVENTION: AND USES THEREOF
8  NUMBER OF SEQUENCES: 1152
9  CORRESPONDENT ADDRESS:
10 ADDRESS: NO. 6292644rtis Corporation
11 STREET: 3054 Cordwainis Road
12 CITY: Research Triangle Park
13 STATE: No. 6292644th Carolina
14 COUNTRY: USA
15 ZIP: 27709
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: F2 3.6.395
20 SOFTWARE: Patent in Release #1.0, Version #1.30
21 CURRENT APPLICATOR DATA:
22 APPLICATOR NUMBER: 6292644
23 FILING DATE: 24-SEP-1997
24 CLASSIFICATION: 445
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: CH 016/97
27 FILING DATE: 31-DEC-1996
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Schindler, J. Timothy
30 REPRESENTATION NUMBER: 38,241
31 REFERENCE TO PARENT APPLICATION: 6292644
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 919-541-8587
34 TELEFAX: 919-541-8689
35 INFORMATION FOR SEQ ID NO: 186:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 615 base pairs
38 TYPE: nucleic acid
39 STRANDEDNESS: single
40 TOPOLOGY: linear
41 MOLECULE TYPE: DNA (genomic)
42 ORIGINAL SOURCE:
43 ORGANISM: PASH074RP
44 US-08-098-416-186

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Matches 43; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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QY 297 GATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 356
DB 486 TGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 545

QY 457 TGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 416
DB 546 TGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 605

QY 417 TTA 419
DB 606 TAA 608

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RESULT 8
US 08-069-046-5/c
Sequence 5, Application US/08069046B
Patent No. 6455762
GENERAL INFORMATION:
APPLICANT: Chiriac, Vincent Lee C.
APPLICANT: Tsai, Chund-Jui

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1  APPLICANT: H. K. Remond
2  TITLE OF INVENTION: Genetic engineering of trans-1,2-diol
3  TITLE OF INVENTION: manipulation of trans-1,2-diol
4  FILE REFERENCE: 981,004081
5  CURRENT FILING DATE: 1997-11-12
6  CURRENT FILING DATE: 1997-11-12
7  NUMBER OF SEQ. ID NOS: 15
8  SOFTWARE: FASTSEQ for Windows Version 5.0
9  SEQ ID NO 5
10 LENGTH: 1172
11 TYPE: DNA
12 ORGANISM: P. falciparum
13 US-08-069-046-5

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QY 575 AAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 576
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RESULT 9
US-09-424-283-5/c
Sequence 5, Application US/09424283
Patent No. 6452219
GENERAL INFORMATION:
APPLICANT: H. K. Remond
TITLE OF INVENTION: Genetic engineering of trans-1,2-diol
FILE REFERENCE: 981,004081
CURRENT FILING DATE: 1997-11-12
CURRENT FILING DATE: 1997-11-12
PRIOR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1998-05-21
DELOF FILING DATE: 1997-05-22
NUMBER OF SEQ. ID NOS: 15
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 5
LENGTH: 1924
TYPE: DNA
ORGANISM: Cytosine max
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BASE/KEY: 015
LOCATION: (119)...(1588)
US-09-424-283-5

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DB 1800 ACTATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1900

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RESULT 10
US 09-570-367-5/c
Sequence 1, Application US/09570367
Patent No. 648881
GENERAL INFORMATION:
APPLICANT: Corcoran, Richard M.
TITLE OF INVENTION: Methods and Compositions for Transferring
FILE REFERENCE: 9579-21

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US-97237,75A
3 FILING DATE: 27 JUN-1997
4 CLASSIFICATION: 435
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Gravello, Michelle
7 REGISTRATION NUMBER: 40,261
8 REFERENCE/KEY NUMBER: 7841-052
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (416) 364 7411
11 TELEFAX: (416) 361-1398
12 INFORMATION FOR SEQ ID NO: 36:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 655 base pairs
15 TYPE: nucleic acid
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: cDNA
19 ORGANISM: Homo sapiens
20 IMMEDIATE SOURCE:
21 CLONE: RH 32
22 US 08 883 795A 36

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Best Local Similarity 47.38; Pred. No. 1.25;
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QY 270 TGAATGCAATATAAACTAAATAGTTGGCTAAAAATTTCTAGCGAAATATCTAGCTAAC 329
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DB 224 TATAAAATTTTAAATATAAAATATTTAAITATAAAATATTTTAAITATAAAATATTTAA 164

QY 330 AAATACCTACTAACTATTAACTAATTTAC*AAAAAATAGCTTAAATTTATTAGT 389
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QY 390 TGGAGCTGTTTGAAGCTTCAACTAAATTTTATAGCAATAAGCTTTTATCTTACGCAATCA 448
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Search completed: December 30, 2002, 21:27:52  
 Job Time : 82 secs



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US-09-323-195A-3
; Sequence 3, Application US/09323195A
; Patent No. 6462257
; GENERAL INFORMATION:
; APPLICANT: Philman, Gerald
; APPLICANT: Cairney, John
; APPLICANT: Perrera, Ranjan
; TITLE OF INVENTION: VICILIN-LIKE SEED STORAGE PROTEIN GENE PROMOTER AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: IPST6006
; CURRENT APPLICATION NUMBER: US/09/323,195A
; CURRENT FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 340
; TYPE: LNA
; ORGANISM: Pinus taeda
US-09-323-195A-3

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Query Match      4.2%; Score 39; Db 4; Length 340;
Best Local Similarity 89.4%; Pred. No. 0.067;
Matches 42; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 ACTATAGGACACGCGTGGTCCACGGCCCGGGCTGGTAAAGTGTGTCG 47

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20010907
2 (bases 1 to 9285)
Jin, Y.
Direct Submission
Submitted (24-MAY-1994) Young-Kwan Jin, Biological Sciences, Purdue
University, 439 Busch Life Science Research Building, West
Lafayette, IN 47907, USA
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Query Match
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Matches 112; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 186 TRGATTCPTGTCGACACVIGLITCTATATTCATTGGAGATATGATGAATAAA 245
DB 17813 TTAAATTCPTTAAGCGCGCAITTTCTAACIAVAVTTGGTTATATTTAGAAATTA 17754

QY 246 TATFRRGVACTTAAGAGAGGTGTTGAAGCAATAAATACTAACTAGTGTGCTAAAA 305
DB 17753 ATGAATCGAAGCTGTTATGCACTTGAAGCTTATAATATGATAATGTAATAGTA 17694

QY 306 TCTTAGTCAAAATATCTAGCTAAVAAATAGCTACTTAACTATTAACATAATTACCAAAA 365
DB 17694 ATTGATTAATAATATCAACACGACCAAAATACATAACCAATAAATAATATAAATA 17634

QY 366 TAACTTAGTAAATATTAAGTTGGGCTGTTCGAAT 403
DB 17633 CTAATCATAGTTAAATAAATAATCTGCAATTATTAATAAT 17596

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Search completed: December 30, 2002, 22:17:41  
Job time : 2998 secs





High quality sequence stop: 631.

## FEATURES

Location/Qualifiers

1..631

SOURCE

Organism "Zea mays"

Zcuffvar "B72"

Zdb\_xref "1400.4577"

Zclone "hs5207"

Zlab\_host "JM107 or DH5a"

Znote "gram: immature ears; site\_1: Xba 1; Site 2: Xba 1;

the vector was digested with XbaI and one nucleotide was

added by fill in the recessive 3' end. The genomic DNA

was nebulized, end repaired, adaptor ligated and size

fractionated using sephadex. The resulting fragments were

between 0.8 and 4 kb and were cloned into the vector

(637 reads in B10p5%, 4674 reads in pUC19). The same

ligation was transformed in either JM107 or DH5a."

BASE COUNT 224 a 105 c 113 g 147 t 2 others

## ORIGIN

Query Match 14.8% Score 146.8; DB 17; Length 631;

Best Local Similarity 87.8%; Prod. No. 66 27; Caps 2;

Matches 172; Conserved 0; Mismatches 22; Indels 2; Gaps 2;

QY 258 TAAGAGAGTGTGTAATGCAATATAAATAATAGTAGTGCT-AAAATGTGTAGTGA 316

DB 464 TTAGAGAGTGTGTAATGCAATATAAATAATAGTAGTGCT-AAAATGTGTAGTGA 405

QY 417 TTAGAGAGTGTGTAATGCAATATAAATAATAGTAGTGCT-AAAATGTGTAGTGA 376

DB 404 TTAGAGAGTGTGTAATGCAATATAAATAATAGTAGTGCT-AAAATGTGTAGTGA 345

QY 477 TTAGAGAGTGTGTAATGCAATATAAATAATAGTAGTGCT-AAAATGTGTAGTGA 436

DB 444 TTAGAGAGTGTGTAATGCAATATAAATAATAGTAGTGCT-AAAATGTGTAGTGA 286

QY 437 TTAGAGAGTGTGTAATGCAATATAAATAATAGTAGTGCT-AAAATGTGTAGTGA 452

DB 285 TTAGAGAGTGTGTAATGCAATATAAATAATAGTAGTGCT-AAAATGTGTAGTGA 270

## RESULT 2

DEFINITION

BB01529 3526\_118\_1B10\_y1\_3526 Recombinant Grid K 3526 mays genomic DNA

sequence.

ACCESSION BB01529

VERSION BB01529.1 GI:22222564

KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 560)

AUTHORS Walbot V.

TITLE Maize genomic sequences found using engineered RecombMu Transposon

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

elide; Panicoidae; Andropogoneae; Zea.

COMMENT 1 (bases 1 to 560)

Walbot V.

Maize genomic sequences found using engineered RecombMu Transposon

Published (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 724 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Very probable ligation site found so sequence was trimmed.

Post ligation sequence submitted separately.

Plate: 3526\_118\_1 row: 24

Class: Transposon-tagged.

Location/Qualifiers

1..560

Organism "Zea mays"

Zcuffvar "B72"

Zdb\_xref "1400.4577"

Zdb\_xref "taxon:177"

Zclone Lib "B72"

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 /dev\_stage "adult"  
 /idb\_host "DH10B"

/note "organ: leaf; Vector: RescuemMu (engineered from pBluescript backbone); Site: 1; BamHI; Site 2: BglII; RescuemMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuemMu, go to the web site 'www.zmbl-labstate.edu' and follow the links for 'RescuemMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 186 a 74 c 100 g 203 t

Query Match 14.4%; Score 135.2; DB 17; Length 560;

Best Local Similarity 81.7%; Pred. No. 5,8626;

Matches 178; Conservative 0; Mismatches 38; Indels 2; Gaps 2;

QY 247 TATTGGGACTTAAAGAGAGTGTGAAATGCAATAAAGAAATATAGTTAGTGGCTAAAAA 305  
 DB 454 TTATGCTGGTTAAGAGATATTGAAATACATGAAATGAAATGAAATGAAATGAAAT 294  
 QY 406 TGTAGTGAATATATCTAGTAAATAGATATGATATGATATGATATGATATGATATG 365  
 DB 293 GTTAGCTGAATATATCTAGTAAATAGATATGATATGATATGATATGATATGATATG 234  
 QY 406 TAAT 425  
 DB 243 TAGTAATAGTAAAT 175  
 QY 426 AACTTTATCTTATGATATCAACATGCGATAGTC 463  
 DB 174 AACTATATGATCTAGTGGATATTAATGATCTTTTATGTC 137

RESULT 4  
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 LOCUS BB216135  
 DEFINITION 1006040E08.y1 1006 - RescuemMu Grid C Zea mays genomic DNA  
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 BB216135  
 VERSION BB216135.1 GI:16806793  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 605)  
 Zea mays genomic sequences found using engineered RescuemMu transposon  
 Walbot V.  
 unpublished (2001)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave,  
 Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu

Very probable ligation site found so sequence was trimmed.  
 Post-ligation sequence submitted separately.  
 Plate: 1006040 row: 46  
 Class: Transposon-tagged.  
 Location/Qualifiers  
 1..605

FEATURES  
 source  
 /organism "Zea mays"  
 /submitter "Zea mays" and W2 V.A.M.B.V."

/dir\_xref "taxon:4577"  
 /clone\_lib "1006 - RescuemMu Grid H"  
 /issue\_type "leaf"  
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 /idb\_host "DH10B"

/note "organ: leaf; Vector: RescuemMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescuemMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuemMu, go to the web site 'www.zmbl-labstate.edu' and follow the links for 'RescuemMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 206 a 118 c 124 g 158 t

Query Match 14.4%; Score 132.8; DB 17; Length 601;

Best Local Similarity 87.5%; Pred. No. 7,6626;

Matches 168; Conservative 0; Mismatches 22; Indels 2; Gaps 2;

QY 254 CATCTACAGAGCTTCAATGCAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 412  
 DB 415 CATCTACAGAGATGTTTAAATGCAATGAAATGAAATGAAATGAAATGAAATGAAAT 474  
 QY 213 GAATTAAT 472  
 DB 475 GAATTAAT 534  
 QY 273 TATTTAAT 432  
 DB 535 TATTTAAT 534  
 QY 433 ATCTTTATATGCA 444  
 DB 594 AGCTCTATATGCA 605

RESULT 5  
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 LOCUS BB84525  
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 qcm-mic clone hw52e07 5', DNA sequence.  
 BB84525  
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 ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Panicoideae; Zea.  
 1 (bases 1 to 458)  
 Zea mays genomic sequences from Zea mays (methyl filtered)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Panicoideae; Zea.  
 1 (bases 1 to 458)  
 Zea mays genomic sequences from Zea mays (methyl filtered)

AUTHORS  
 Richard McCombie  
 Lila Auerberg Hazen Genomic Sequencing Center  
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 Po Box 100, Cold Spring Harbor, NY 11724, USA  
 Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: mcombie@cshl.org  
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 Seq primer: -21M30invFwd  
 Class: shotgun  
 High quality sequence step: 458.  
 Location/Qualifiers  
 1..458





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/dev_stage "adult"
/lab_host "dh10b"
/notes "organ: leaf; Vector: RescuerMu (engineered from
pBlueScript backbone); Site: BamHI; Site: 2; BamHI;
RescuerMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescuerMu, go to the web
site www.zmh.hastate.edu and follow the links for
'RescuerMu.' Grid 1 was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BamHI, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
BASE COUNT      207 a      88 c      95 g      188 t
ORIGIN

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```

Query Match      13.8%; Score 127.2; DB 17; Length 578;
Best Local Similarity 82.8%; Pred. No. 2.7e-24;
Matches 169; Conservative 0; Mismatches 33; Indels 2; Gaps 2;

QY 258 TAACGAGTGTTCACGACAAATACAACTAATAGTTAGTTGGCT-AAAATGTTAGTGA 316
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 232 TAACGAGTGTTCGAAATGATGACAACTAATAGTTAGTTAGTTAGTAAATAGTAA 291
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 417 TTATCTAGCTTACAAATAGTACCTAATTAATTAATTAATTAATTAATTAATTAAT 376
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 294 TTATCTAGTTAATAAAGATATATTAATTAATTAATTAATTAATTAATTAATTAAT 351
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 477 TAAATATTAAATTTGGCTGTGTTGAATGCTCACTAATTTTAGCCACTTAATTTTATCT 436
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 452 TGAATCTAT-AGATAGATGTTTGTGATGTTGCACTAATTTTAGACACTTAATTTAT 419
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 437 TTATCTAGTTACCAACATGCAATAA 460
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 411 CTACTGATTCACCAACATGCAATAA 434
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 8
LOCUS      BH216415
DEFINITION 1096041307.y1.1036 - RescuerMu Grid G Zea mays genomic DNA
sequence.
ACCESSION  BH216415
VERSION     BH216415.1 GI:16806973
KEYWORDS   GSS.
SOURCE      Zea mays.
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACB
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 591)
            Waldbert V.
            Maize genomic sequences found using engineered RescuerMu transposon
            unpublished (2001)
            Contact: Waldbert V.
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: waldbert@stanford.edu
            Very probable ligation site of ends cut by single endonuclease.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1006041 row: 4E
            Class: transposon-tagged.
            Location/Qualifiers
                location=1..591
                organism="Zea mays"
                project="Grid G and W1, W2, W3, W4, W5"
                submitter="Waldbert V."
                Zebase="1006041307"
                Zclone="Lib 1006 - RescuerMu Grid G"
                Ztissue_type="leaf"

```

```

FEATURES
            source
            location/Qualifiers
                location=1..591
                organism="Zea mays"
                project="Grid G and W1, W2, W3, W4, W5"
                submitter="Waldbert V."
                Zebase="1006041307"
                Zclone="Lib 1006 - RescuerMu Grid G"
                Ztissue_type="leaf"

```

```

/dev_stage "adult"
/lab_host "dh10b"
/notes "organ: leaf; Vector: RescuerMu (engineered from
pBlueScript backbone); Site: BamHI; Site: 2; BamHI;
RescuerMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescuerMu, go to the web
site www.zmh.hastate.edu and follow the links for
'RescuerMu.' Grid 1 was grown at Stanford in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BamHI, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
BASE COUNT      203 a      115 c      121 g      352 t
ORIGIN

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Query Match      13.7%; Score 126.4; DB 17; Length 591;
Best Local Similarity 87.5%; Pred. No. 4.5e-24;
Matches 161; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

QY 254 CACTTAACGAGTGTTCGAAATGCAATACAAATTAATAGTTAGTTAGT-AAAAATTTATAT 312
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 458 CAGCAAGAGAGATGTTTAATAGCACTAGATTAATAGTTAGTTAGTAA-AAAAAAATTTATAT 467
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 413 GAAATATTCTAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 472
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 468 GAAATATTCTAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 527
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 373 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 482
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 528 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 596
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 433 ATCT 436
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 587 AGCT 590
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 9
LOCUS      BH775726
DEFINITION 12mbol11016d10 12mb, filtered library Zea mays genomic clone
sequence.
ACCESSION  BH775726
VERSION     BH775726.1 GI:19777941
KEYWORDS   GSS.
SOURCE      Zea mays.
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACB
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 590)
            Rudman, M.A., Freese, R.G., Baskin, J.A., Nanda, J.A., and Lukens, L.J.
            Genome-wide methylation filtered genomic sequences from maize
            unpublished (2002)
            Contact: Redell JA
            erican Genomics, LLC
            4941 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jredell@erican-genomics.com
            Plate: 12mbol11016 row: a column: 1b
            Seq primer: M13 forward
            Class: shotgun
            Biol. quality sequence stop: 590.
            Location/Qualifiers
                location=1..590
                organism="Zea mays"
                project="H017"
                submitter="Waldbert V."
                Zebase="100604577"
                Zclone="Lib 12mbol11016d10"
                Ztissue_type="leaf"
                Zvector="pB-SE"
                Zseq_type="H017"

```

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FEATURES
            source
            location/Qualifiers
                location=1..590
                organism="Zea mays"
                project="H017"
                submitter="Waldbert V."
                Zebase="100604577"
                Zclone="Lib 12mbol11016d10"
                Ztissue_type="leaf"
                Zvector="pB-SE"
                Zseq_type="H017"

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QY 254 CACTAAGGAGTGTGTTGAAGCAATAAAGAACTAATAGTTAGTGGCTAAATATGT--TAG 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 427 CACTAAGGAGTGTGTTGAAGCAATAAAGAACTAATAGTTAGTGGCTAAATATGTGCTAG 486

QY 312 TGAATATATCTAG-CTAACAATAAGCTAGCTAATCTAATTAACCTAATTTAGCAAAAATACT 370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 487 TGAATATATCTAGCTAAGCAATAAGCTAATCTAATTAACCTAATTTAGCAAAAATACT 546

QY 471 TATAGTTAAATATTAAGTTGGGCTGTTTGAATGCTCAACTAATTTAGGCACTAATCTT 430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 547 AATAG-IAAAGCTAATAGCTAGTGGG-GTTTGAATGCTCAACTAATTTAGGCACTAACTA 605

QY 431 TTATCTATAGTGCATCAAAACA 452
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 606 TTATCTATAGTGCATCAAAACA 627

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RESULT 12
HH010577-
LOCUS HH01057 437 bp DNA linear GUS 25-APR 2002
DEFINITION HH01057 - RescuedMu Grid 1 Zea mays genomic DNA
SEQUENCE
HH01057
VERSION HH01057.1 GI:20313738
KEYWORDS GUS.
SOURCE Zea mays.
ORGANISM Zea mays.

```

```

REFERENCE
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescuedMu Transposon
JOURNAL Unpublished (2001)
COMMENT Department of Biological Sciences
Stanford University
865 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

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```

Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1008113 row: 38
Class: transposon-tagged.
Location/Qualifiers
    1..337
        /organism="Zea mays"
        /contig="us-10-039-836a-3.rst"
        /date="2002-04-25"
        /db_xref="taxon:4577"
        /feature="1"
        /feature_type="CDS"
        /dev_stage="adult"
        /lab_host="DH10B"
        /note="organ: leaf; Vector: RescuedMu (engineered from
        pBluescript backbone); Site_1: BamHI; Site_2: BglII;
        RescuedMu is a 4.9 kb, modified maize Mu transposon
        designed to allow plasmid rescue from total genomic DNA.
        Mu elements insert preferentially into transcription
        units. For more information on RescuedMu, go to the web
        site www.zmdb.berkeley.edu and follow the links for
        'RescuedMu.' Grid 1 was grown at Berkeley in 2001. DNA was
        extracted from leaf punches, double digested using BamHI
        and BglII, and ligated to form circular plasmids. DH10B
        cells were transformed and then screened on LB plates with
        ampicillin."

```

```

BASE COUNT 112 a 31 c 55 g 139 t
ORIGIN
Query Match 13.9%; Score 119.8; DB 17; Length 337;
Best Local Similarity 82.6%; Pred. No. 2,60-22;
Matches 141; Conservative 0; Mismatches 32; Indels 2; Gaps 2;

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QY 242 TAAA-TAATGAGGAGTGTGTTGAAGCAATAAAGAACTAATAGTTAGTGGCTAAATATGT 402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 TAAA-TAATGAGTGTGTTGAAGCAATAAAGAACTAATAGTTAGTGGCTAAATATGTAGCTA 141

QY 302 AAAT-TGTTCAGTAAATATCTAGCTAATCTAATTAACCTAATTTAGCAAAAATACT 500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 AAAA-TATTAAGTAAATTAACCTAATCTAATTAACCTAATTTAGCAAAAATACT 81

QY 361 AAAAATAA-TATTAAGTAAATATCTAGCTAATCTAATTAACCTAATTTAGCAAAAATACT 429
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 AAAAATAA-TATTAAGTAAATATCTAGCTAATCTAATTAACCTAATTTAGCAAAAATACT 22

QY 421 CCACTAATCTTTATC 435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 CCACTAATCTTTATC 7

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RESULT 13
HH224384
LOCUS HH224384 1061 bp DNA linear GUS 25-APR 2002
DEFINITION HH224384 - RescuedMu Grid 3 Zea mays genomic DNA
SEQUENCE
HH224384
VERSION HH224384.1 GI:16821259
KEYWORDS GUS.
SOURCE Zea mays.
ORGANISM Zea mays.

```

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REFERENCE
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescuedMu Transposon
JOURNAL Unpublished (2001)
COMMENT Department of Biological Sciences
Stanford University
865 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

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Very probable ligation site of ends cut by shuttle enzyme.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006118 row: 43
Class: transposon-tagged.
Location/Qualifiers
    1..508
        /organism="Zea mays"
        /contig="us-10-039-836a-3.rst"
        /date="2002-04-25"
        /db_xref="taxon:4577"
        /feature="1"
        /feature_type="CDS"
        /dev_stage="adult"
        /lab_host="DH10B"
        /note="organ: leaf; Vector: RescuedMu (engineered from
        pBluescript backbone); Site_1: BamHI; Site_2: BglII;
        RescuedMu is a 4.9 kb, modified maize Mu transposon
        designed to allow plasmid rescue from total genomic DNA.
        Mu elements insert preferentially into transcription
        units. For more information on RescuedMu, go to the web
        site www.zmdb.berkeley.edu and follow the links for
        'RescuedMu.' Grid 3 was grown at Stanford in 2000. DNA was
        extracted from leaf punches, double digested using BamHI
        and BglII, and ligated to form circular plasmids. DH10B
        cells were transformed and then screened on LB plates with
        ampicillin."

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BASE COUNT 186 a 106 c 75 g 141 t
ORIGIN
Query Match 12.9%; Score 119.4; DB 17; Length 508;
Best Local Similarity 86.7%; Pred. No. 3,80-22;
Matches 143; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

```



|||||  
DB 385 AATTCAAATCTCATAGCTCAAGACTAAAGCTTTGTGGAGGCT 431

Search completed: December 30, 2002, 22:50:17  
Job time : 2160 secs



Request No.	Score	Query Match	Length	DB	ID	Description
1	40.6	4.4	2000	9	US-09-938-842A-5309	Sequence 5309, Appli
2	49.2	4.3	640681	13	US-09-790-998-1	Sequence 5, Appli
3	49.8	4.3	1188	9	US-10-051-307-5	Sequence 197, App
4	48.6	4.2	334	10	US-09-964-373-197	Sequence 198, App
5	48.5	4.2	334	10	US-09-964-373-198	Sequence 4, Appli
6	38.2	4.1	1175	9	US-10-051-307-4	Sequence 1, Appli
7	48	4.1	2791	9	US-09-617-278-1	Sequence 1, Appli
8	48	4.1	2791	10	US-09-915-524-1	Sequence 1, Appli
9	48	4.1	2791	10	US-09-938-634-1	Sequence 1, Appli
10	47.8	4.1	2194	10	US-09-811-033-43	Sequence 43, Appli
11	47.6	4.1	985	10	US-09-811-093-44	Sequence 44, Appli
12	47.6	4.1	1872	9	US-09-938-842A-5304	Sequence 3, Appli
13	47.6	4.1	53332	10	US-09-938-842A-5304	Sequence 3, Appli
14	47.4	4.0	643631	10	US-09-938-842A-5304	Sequence 3, Appli
15	47.2	4.0	2611	9	US-09-891-139A-1	Sequence 1, Appli
16	47.2	4.0	2745	9	US-09-891-139A-1	Sequence 1, Appli
17	47	4.0	2000	9	US-09-938-842A-4650	Sequence 4650, App
18	47	4.0	2240	9	US-09-938-842A-4650	Sequence 16, Appli
19	46.6	4.0	594	9	US-09-938-842A-4650	Sequence 16, Appli

1608 THE PATENT

[illegible]





Matches 41; conservative 0; Mismatches 1.

RESULTS 7  
 US-09 917 378 1/3  
 : Sequence 1, Application US/09/17278  
 : Patent No. US2002016866A1  
 : GENERAL INFORMATION:  
 : APPLICANT: GORZYNSKI, ROBERT M.  
 : TITLE OF INVENTION: CLARK, DAVID A.  
 : FILE REFERENCE: 9579-39  
 : CURRENT APPLICATION NUMBER: 09/17278  
 : CURRENT FILING DATE: 2001-07-30  
 : PRIOR APPLICATION NUMBER: 60/064,764  
 : PRIOR FILING DATE: 1997-11-07





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CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;  
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 600 BP: 177 A; 97 C; 110 G; 215 T; 1 other;

Query Match 4.6%; Score 42.6; DB 23; Length 600;  
 Best Local Similarity 54.9%; Prev. No. 0.11;  
 Matches 61; Conservative 0; Mismatches 69; Indels 0; Gaps 0;  
 QY 233 TGAATGAAATAATATGGAACATTAAGGAGGTGTTCAATGCAATAAAGCTAAATAGTT 292  
 DB 496 TGAATGAAATAATATGGAACATTAAGGAGGTGTTCAATGCAATAAAGCTAAATAGTT 292  
 QY 293 AATGCTAAATATGTAAGCAATATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 352  
 DB 436 TGTTCCTATATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 352  
 QY 437 AATGCTAAATATGTAAGCAATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 377  
 DB 476 AATGCTAAATATGTAAGCAATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 377

## RESULT 14

AB134495/2  
 ID AB134495 standard; DNA: 18817 BP.

AC A6134495;  
 DT 01-JUN-2002 (first entry)

DE Chemically treated cell signalling DNA sequence complementary to 26.  
 XX Cell signalling; cytosine methylation; cell signalling disease;  
 KW cancer; tumor; cytostatic; ds.  
 XX Undisrupted.  
 XX W020017476-A2.  
 XX 10 JAN 2002.  
 XX 29 JUN 2001; 2001W0-EP07471.  
 XX 30 JUN 2000; 2000DE-1042529.  
 XX 01 SEP 2000; 2000DE-1043826.  
 XX (EP16-) EPIGENOMICS AG.  
 XX clock A. Pispach; C. Roth; K.  
 XX WPI: 2002-154759/20.  
 XX Nucleic acid, useful for diagnosis and therapy of diseases associated  
 XX with cell signalling e.g. cancer, comprises chemically modified genomic  
 XX sequences of genes associated with cell signalling.  
 XX Claim 1: SEQ ID No 52; 24pp-sequence listing; English.  
 XX The invention relates to a nucleic acid comprising a sequence of at least  
 XX 18 bases of a segment of chemically pretreated DNA of genes associated  
 XX with cell signalling. The activity of the modified sequences of the  
 XX invention may be described as cytostatic. The object of the invention is  
 XX to provide the chemically modified DNA of genes associated with cell

CC signalling, as well as oligonucleotides and/or DNA elements for  
 CC detecting cytosine methylations, as well as a method which is  
 CC particularly suitable for the diagnosis and/or therapy of tumors and  
 CC epigenetic parameters of genes associated with cell signalling. The  
 CC chemically modified DNA provided by the invention is useful for diagnosis  
 CC and therapy of diseases such as solid tumors and cancer. The sequences  
 CC given in records AB134495-AB134496 represent chemically pretreated  
 CC genomic DNA's of genes associated with cell signalling.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but is based on sequence information supplied by the  
 XX European Patent Office.

XX Sequence 18817 BP: 5486 A; 156 C; 350 G; 967 T; 1 other;

Query Match 4.6%; Score 42.6; DB 24; Length 18817;  
 Best Local Similarity 48.2%; Prev. No. 0.45;  
 Matches 120; Conservative 0; Mismatches 125; Indels 0; Gaps 0;  
 QY 218 TTTCATTCACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 277  
 DB 12942 TTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 12942  
 QY 278 ATAAATTAATAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 337  
 DB 12872 ATAAATTAATAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 337  
 QY 338 AATTAATTAATAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 397  
 DB 12812 AATTAATTAATAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 397  
 QY 398 TTCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 457  
 DB 12752 TTCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 457  
 QY 458 TAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 517  
 DB 12692 TAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 517

## RESULT 14

AB134495/2  
 ID AB134495 standard; DNA: 18817 BP.

AC A6134495;  
 DT 26-MAR-2002 (first entry)

DE Human metastasis associated gene SEQ ID No 18.  
 XX Metastasis associated gene; cytosine methylation; gene; ds.  
 KW cytosine methylation; gene; ds.  
 XX Homo sapiens.  
 XX W020017476-A2.  
 XX 18-OCT-2001.  
 XX 06-APR-2001; 2001W0-EP04970.  
 XX 06-APR-2000; 2000DE-1019058.  
 XX 07-APR-2000; 2000DE-1019173.  
 XX 30-JUN-2000; 2000DE-1032529.  
 XX 01-SEP-2000; 2000DE-1043826.  
 XX (EP16-) EPIGENOMICS AG.  
 XX clock A. Pispach; C. Roth; K.  
 XX WPI: 2002-154759/20.  
 XX Nucleic acid derived from chemically treated metastasis genes,  
 XX useful for diagnosis of cancers by analysis of cytosine methylation

